Amendments to the Specification

Please insert the following paragraph at page 10, line 11:

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

Please insert the following paragraph at page 10, line 14:

Figure 2. Consensus alignments carried out using ICM (Molsoft LLC, La Jolla, CA) between human GR (glucocorticoid receptor) LBD and other human NHR LBDs, indicating by shading the residues of Site II, i.e. residues corresponding to residues of GR Site II. Dots are spaceholders and do not represent amino acids. Numbers refer to the first residue in each line, are specific for each NHR and are based on the full-length NHR. For the NHRs listed below, with the exception of GR and MR, structural data was obtained from the RCSB references listed below, and the numbering system in the RCSB references was used. For GR and MR, structural data was obtained by homology modeling using the literature references below, and the numbering system in those literature references was used. The RCSB references (in parentheses) and literature references for the various NHRs are as follows:

RXRalpha (SEQ ID NO:3) (1lbd) Bourguet, W., Ruff, M., Chambon, P., Gronemeyer, H., Moras, D. Nature 375 pp. 377 (1995); PPAR-gamma (~~SEQ ID NO:4~~ SEQ ID NO:10) (2prg) Nolte, R. T., Wisely, G. B., Westin, S., Cobb, J. E., Lambert, M. H., Kurokawa, R., Rosenfeld, M. G., Willson, T. M., Glass, C. K., Milburn, M. V. Nature 395 pp. 137 (1998); RARgamma (~~SEQ ID NO:5~~ SEQ ID NO:4) (2lbd) Renaud, J. P., Rochel, N., Ruff, M., Vivat, V., Chambon, P., Gronemeyer, H., Moras, D. Nature 378 pp. 681 (1995); PR (~~SEQ ID NO:6~~ SEQ ID NO:5) (1a28) Williams, S. P., Sigler, P. B. Nature 393 pp. 392 (1998); VitDR (~~SEQ ID NO:7~~ SEQ ID NO:9) (1db1) Rochel, N., Wurtz, J. M., Mitschler, A., Klaholz, B., Moras, D. Mol. Cell 5 pp. 173 (2000); AR (~~SEQ ID NO:8~~ SEQ ID NO:6) (1e3g) Matias, P. M., Donner, P., Coelho, R., Thomaz, M., Peixoto, C., Macedo, S., Otto, N., Joschko, S., Scholz, P., Wegg, A., Basler, S., Schafer, M., Egner, U., Carrondo, M. A. J.Biol.Chem. 275 pp. 26164 (2000); ERalpha (~~SEQ ID NO:9~~ SEQ ID NO:7) (1a52) Tanenbaum, D. M., Wang, Y., Williams, S. P., Sigler, P. B. Proc Natl Acad Sci U S A 95 pp. 5998 (1998); ERbeta (~~SEQ ID NO:10~~ SEQ ID NO:8) (1l2j) Shiau,

A. K., Barstad, D., Radek, J. T., Meyers, M. J., Nettles, K. W., Katzenellenbogen, B. S., Katzenellenbogen, J. A., Agard, D. A., Greene, G. L. Nat.Struct.Biol. 9 pp. 359 (2002); TRbeta (~~SEQ ID NO:11~~ SEQ ID NO:12) (1bsx) Wagner, R. L., Darimont, B. D., Apriletti, J. W., Stallcup, M. R., Kushner, P. J., Baxter, J. D., Fletterick, R. J., Yamamoto, K. R. Genes Dev. 12 pp. 3343 (1998). MR and GR structural data were obtained by homology modeling to PR using the sequences from the following references: GR (~~SEQ ID NO:12~~ SEQ ID NO:13), PIR Accession Number QRHUGA, Hollenberg, S.M., Weinberger, C., Ong, E.S., Cerelli, G.,Oro, A., Leba, R., Thompson, E.B., Rosenfeld, M.G., Evans, R.M. Nature (1985) 318: 635-641; MR (~~SEQ ID NO:13~~ SEQ ID NO:11), PIR Accession Number A29613, Arriza, J.L.; Weinberger, C., Cerelli, G., Glaser, T.M., Handelin, B.L., Housman, D.E., Evans, R.M., Science (1987) 237: 268-275..

Please insert the following paragraph at page 12, line 8:

Various computational analyses are therefore necessary to determine whether a molecule or a portion thereof is sufficiently similar to all or parts of the disclosed homology model to be considered equivalent. Such analyses may be carried out in current software applications, such as InsightII (Accelrys Inc., San Diego, CA) Version 2000 as described in the User's Guide, online (~~www.accelrys.com~~) or software applications available in the SYBYL software suite (Tripos Inc., St. Louis, MO).

Please insert the following paragraph at page 75, line 28:

The fifty-one compounds used in the following examples were synthesized as follows. These compounds and their synthesis are described in the co-pending provisional application entitled "Modulators of the Glucocorticoid Receptor and Method," ~~attorney docket number QA266PSP,~~ U.S. Application No. 60/396,877, filed on July 18, 2002, and in co-pending utility application entitled "Modulators of the Glucocorticoid Receptor and Method," ~~attorney docket number QA266NP,~~ U.S. Application No.[[_____]] 10/621,909, filed concurrently herewith. The contents of U.S. Application No. 60/396,877 and QA266NP are incorporated herein by reference in their entirety.

Please insert the following paragraph at page 96, line 6:

The GR homology model of the ligand binding domain (LBD) was constructed using known methodology. Specifically, the human sequence (QRHUGA obtained from the International Protein Sequence Database, pir.georgetown.edu/pirwww), residues 523-777 (SEQ ID NO:1), comprising the LBD was aligned to the human PR sequence (LBD residues 682-932) (SEQ ID NO:2) available as a xray-structure (1A28.pdb obtained from the RCSB, the Research Collaboratory for Structural Bioinformatics, www.rcsb.org/pdb) using the modeler module within InsightII (Version 2000, MSI/Accelrys).

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GR:   523 ATLPQLTPTLVSLLEVIEPEVLYAGYDSSVPDSTWRIMTTLNMLGGRQVI 572
1A28: 682     QLIPPLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLL 727


GR:   573 AAVKWAKAIPGFRNLHLDDQMTLLQYSWMFLMAFALGWRSYRQSSANLLC 622
1A28: 728 SVVKWSKSLPGFRNLHIDDQITLIQYSWMSLMVFGLGWRSYKHVSGQMLY 777


GR:   623 FAPDLIINEQRMTLPCMYDQCKHMLYVSSELHRLQVSYEEYLCMKTLLLL 672
1A28: 778 FAPDLILNEQRMKESSFYSLCLTMWQIPQEFVKLQVSQEEFLCMKVLLLL 827


GR:   673 SSVPKDGLKSQELFDEIRMTYIKELGKAIVKRE-GN-SSQNWQRFYQLTK 720
1A28: 828 NTIPLEGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVSSS--QRFYQLTK 875


GR:   721 LLDSMHEVVENLLNYCFQTFLDKTM-SIEFPEMLAEIITNQIPKYSNGNI 769
1A28: 876 LLDNLHDLVKQLHLYCLNTFIQSRALSVEFPEMMSEVIAAQLPKILAGMV 925


GR:   770 KKLLFHQK 777    (SEQ ID NO:1)
1A28: 926 KPLLFH-K 932    (SEQ ID NO:2)
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Please insert the following paragraph at page 99, line 1:

Table II. Correlation Data for Analogues of Compound 15

Please insert the following paragraph at page 109, line 29:

Table I. GR Homology Model Coordinates (SEQ ID NO:1)

Please insert the following paragraph at page 157, line 20:

<u>Table III. Structure Coordinates for Site II in Various NHRs</u>

<u>Based on the Consensus Alignments in Figure 2</u>

Please insert the following paragraph at page 157, line 21:

AR Site II Residues (ref. 1E3G.pdb) <u>(highlighted residues of SEQ ID NO:6)</u>

Please insert the following paragraph at page 164, line 26:

ERalpha Site II Residues (ref. 1A52.pdb) <u>(highlighted residues of SEQ ID NO:7)</u>

Please insert the following paragraph at page 171, line 26:

ERbeta Site II Residues (ref. 1L2J.pdb) <u>(highlighted residues of SEQ ID NO:8)</u>

Please insert the following paragraph at page 178, line 21:

GR Homology Model Site II Residues (ref. GR_icm_aligned.pdb) <u>(highlighted redidues of SEQ ID NO:13)</u>

Please insert the following paragraph at page 185, line 31:

MR Homology Model Site II Residues (ref. MR_homo.pdb) <u>(highlighted residues of SEQ ID NO:11)</u>

Please insert the following paragraph at page 193, line 6:

PPARgamma Site II Residues (ref. 2PRG.pdb) <u>(highlighted residues of SEQ ID NO:10)</u>

Please insert the following paragraph at page 200, line 26:

PR Site II Residues (ref. 1A28.pdb) <u>(highlighted residues of SEQ ID NO:5)</u>

Please insert the following paragraph at page 207, line 35:

RARgamma Site II Residues (ref. 2LBD.pdb) <u>(highlighted residues of SEQ ID NO:4)</u>

Please insert the following paragraph at page 216, line 26:

RXRalpha Site II Residues (ref. 1LBD.pdb) (highlighted residues of SEQ ID NO:3)

Please insert the following paragraph at page 223, line 35:

TRbeta Site II Residues (ref. 1BSX.pdb) (highlighted residues of SEQ ID NO:12)

Please insert the following paragraph at page 231, line 4:

VitDR Site II Residues (ref. 1DB1.pdb) (highlighted residues of SEQ ID NO:9)

Please insert the following paragraph at page 238, line 29:

Table IV. GR Homology Model Coordinates (SEQ ID NO:1) discerned from the disclosure in WO 03/015692 A2

Please insert the following paragraph at page 246, line 21:

Table V. GR Homology Model Coordinates (SEQ ID NO:1) discerned from the disclosure in Kauppi et. al.